

Resource Summary Report

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ChIP-seq

RRID:SCR_001237

Type: Tool

Proper Citation

ChIP-seq (RRID:SCR_001237)

Resource Information

URL: <https://gitlab.sib.swiss/EPD/chipseq>

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Description: Set of software modules for performing common ChIP-seq data analysis tasks across the whole genome, including positional correlation analysis, peak detection, and genome partitioning into signal-rich and signal-poor regions. The tools are designed to be simple, fast and highly modular. Each program carries out a well-defined data processing procedure that can potentially fit into a pipeline framework. ChIP-Seq is also freely available on a Web interface.

Abbreviations: ChIP-seq

Synonyms: ChIP-seq - Tools for the analysis of ChIP-seq data

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Defining Citation: [PMID:27863463](#)

Keywords: high-throughput sequencing, chromatin immuno precipitation, chip-seq, genome, c

Availability: Free, Available for download, Freely available

Resource Name: ChIP-seq

Resource ID: SCR_001237

Alternate IDs: OMICS_02103

Alternate URLs: <https://epd.expasy.org/chipseq/>, <https://chip-seq.sourceforge.net/>

License: GNU General Public License, v3

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260905T132431+0000

Ratings and Alerts

No rating or validation information has been found for ChIP-seq.

No alerts have been found for ChIP-seq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8035 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

Yang L, et al. (2026) Transcription factor ATF3 aggravates kidney fibrosis by maintaining the state of histone H3 lysine 27 acetylation. Chinese medical journal, 139(2), 253.

Atri Roozbahani G, et al. (2026) Induction of cellular senescence by androgen receptor agonist or antagonist is mediated via two novel common DYRK1A-DREAM and cyclin G2 signaling pathways in castration-resistant prostate cancer. Journal of advanced research, 80, 371.

Hossain M, et al. (2026) ChromAcS: an automated and flexible GUI for end-to-end reproducible ATAC-seq analysis across multiple species. BMC bioinformatics, 27(1).

Wang D, et al. (2026) WDR5 remodels NANOG condensates to drive transcriptional programs and sustain stem cell identity. Nature communications, 17(1).

Gao Z, et al. (2026) Photoclick chemistry led to the identification of HELLS as a helicase for DNA G-quadruplexes. Nucleic acids research, 54(3).

Cui W, et al. (2026) Protease-mediated PRC1 dissociation promotes H2AK119ub remodeling during stress responses. The EMBO journal, 45(8), 2561.

Kok JY, et al. (2026) Nucleosome positioning shapes cryptic antisense transcription. PLoS genetics, 22(3), e1012078.

Amaral ML, et al. (2026) Single-cell epigenomics uncovers heterochromatin instability and transcription factor dysfunction during mouse brain aging. Cell reports, 45(3), 117073.

Chen B, et al. (2026) NRIP1 disrupts ER α signal in Sjögren's disease via AQP5 suppression and MYC-driven salivary dysfunction. Experimental & molecular medicine, 58(3), 898.

Kuliński TM, et al. (2026) DIS3 mutations enhance AID-driven translocations during B-cell activation, promoting transformation to multiple myeloma. *Nature communications*, 17(1).

Abbas A, et al. (2026) Accurate prediction of cohesin and RNA Polymerase II-associated chromatin interactions using convolutional neural networks. *Nucleic acids research*, 54(6).

van Schendel R, et al. (2026) TONSL suppresses polymerase theta-dependent tandem duplications through chromatin-guided repair. *Nature communications*, 17(1).

Yu YH, et al. (2026) CRM-TI: an enhanced pipeline for computationally assigning the target genes of cis-regulatory modules by considering comprehensive long-range regulation mechanisms. *BioData mining*, 19(1).

Bidany-Mizrahi T, et al. (2026) WWOX maintains epidermal identity and suppresses EMT to prevent aggressive cutaneous squamous cell carcinoma. *Proceedings of the National Academy of Sciences of the United States of America*, 123(16), e2534844123.

Hamm DC, et al. (2026) KLF18 is a necessary component of the DUX4-initiated transcriptional network and a candidate locus for phenotypic diversity. *Genes & development*, 40(11-12), 873.

Su Y, et al. (2026) Sequential transcriptional waves and NF- κ B-driven chromatin remodeling direct drug-induced dedifferentiation in cancer. *Nature communications*, 17(1).

Garcia-Urena M, et al. (2026) Genome-Wide Discovery Reveals Adipose-Specific and Systemic Regulators of Insulin Resistance. *medRxiv : the preprint server for health sciences*.

Xu H, et al. (2026) Postnatal conversion of methylcytosine to hydroxymethylcytosine reconfigures the human neuronal epigenome. *bioRxiv : the preprint server for biology*.

Saito R, et al. (2026) Decoding the molecular logic of rapidly evolving ZAD zinc finger proteins in *Drosophila*. *Science advances*, 12(9), eady7568.

Luo YN, et al. (2026) A de novo H3.2K9me2 deposition pathway establishes heterochromatin for suppressing transposon mobilization during fly somatic development. *Nucleic acids research*, 54(5).